

# Xavier Soberon

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10873099/publications.pdf>

Version: 2024-02-01

59  
papers

3,274  
citations

257450

24  
h-index

161849

54  
g-index

61  
all docs

61  
docs citations

61  
times ranked

6576  
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole genome variation in 27 Mexican indigenous populations, demographic and biomedical insights. PLoS ONE, 2021, 16, e0249773.	2.5	8
2	Association of FAAH p.Pro129Thr and COMT p.Ala72Ser with schizophrenia and comorbid substance use through next-generation sequencing: an exploratory analysis. Revista Brasileira De Psiquiatria, 2021, , .	1.7	2
3	Variation in Actionable Pharmacogenetic Markers in Natives and Mestizos From Mexico. Frontiers in Pharmacology, 2019, 10, 1169.	3.5	15
4	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. Nature, 2019, 570, 71-76.	27.8	248
5	Microbiome-MX 2018: microbiota and microbiome opportunities in Mexico, a megadiverse country. Research in Microbiology, 2019, 170, 235-241.	2.1	2
6	Exploratory Analysis of Rare and Novel Variants in Mexican Patients Diagnosed with Schizophrenia and Dementia. Revista De Investigacion Clinica, 2019, 71, 246-254.	0.4	4
7	Identification and characterization of Taenia solium enolase as a plasminogen-binding protein. Acta Tropica, 2018, 182, 69-79.	2.0	19
8	Fate of uptaken host proteins in Taenia solium and Taenia crassiceps cysticerci. Bioscience Reports, 2018, 38, .	2.4	11
9	Prediction of atorvastatin plasmatic concentrations in healthy volunteers using integrated pharmacogenetics sequencing. Pharmacogenomics, 2017, 18, 121-131.	1.3	16
10	Demographic history and biologically relevant genetic variation of Native Mexicans inferred from whole-genome sequencing. Nature Communications, 2017, 8, 1005.	12.8	44
11	A Loss-of-Function Splice Acceptor Variant in IGF2 Is Protective for Type 2 Diabetes. Diabetes, 2017, 66, 2903-2914.	0.6	52
12	Experimental and Theoretical Approaches To Investigate the Immunogenicity of Taenia solium-Derived KE7 Antigen. Infection and Immunity, 2017, 85, .	2.2	7
13	Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. Cell, 2017, 170, 199-212.e20.	28.9	121
14	Pharmacogenetic Variation in Over 100 Genes in Patients Receiving Acenocumarol. Frontiers in Pharmacology, 2017, 8, 863.	3.5	7
15	Quantitative multiplexed proteomics of Taenia solium cysts obtained from the skeletal muscle and central nervous system of pigs. PLoS Neglected Tropical Diseases, 2017, 11, e0005962.	3.0	12
16	Role of porcine serum haptoglobin in the host-parasite relationship of Taenia solium cysticercosis. Molecular and Biochemical Parasitology, 2016, 207, 61-67.	1.1	10
17	Exploring Variation in Known Pharmacogenetic Variants and its Association with Drug Response in Different Mexican Populations. Pharmaceutical Research, 2016, 33, 2644-2652.	3.5	16
18	Genome analysis of Excretory/Secretory proteins in Taenia solium reveals their Abundance of Antigenic Regions (AAR). Scientific Reports, 2015, 5, 9683.	3.3	54

#	ARTICLE	IF	CITATIONS
19	Genotype frequencies of VKORC1 and CYP2C9 in Native and Mestizo populations from Mexico, potential impact for coumarin dosing. <i>Gene</i> , 2015, 558, 235-240.	2.2	15
20	Combining metagenomics, metatranscriptomics and viromics to explore novel microbial interactions: towards a systems-level understanding of human microbiome. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 390-401.	4.1	182
21	Association of a Low-Frequency Variant in <i>HNF1A</i> With Type 2 Diabetes in a Latino Population. <i>JAMA - Journal of the American Medical Association</i> , 2014, 311, 2305.	7.4	230
22	The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. <i>Science</i> , 2014, 344, 1280-1285.	12.6	420
23	The genomes of four tapeworm species reveal adaptations to parasitism. <i>Nature</i> , 2013, 496, 57-63.	27.8	603
24	Alternative Splice Variants in TIM Barrel Proteins from Human Genome Correlate with the Structural and Evolutionary Modularity of this Versatile Protein Fold. <i>PLoS ONE</i> , 2013, 8, e70582.	2.5	7
25	Evolutionary Walk between $(\beta/\beta)_8$ Barrels: Catalytic Migration from Triosephosphate Isomerase to Thiamin Phosphate Synthase. <i>Journal of Molecular Biology</i> , 2012, 416, 255-270.	4.2	17
26	Exploring the Structure-Function Loop Adaptability of a $(\beta/\beta)_8$ -Barrel Enzyme through Loop Swapping and Hinge Variability. <i>Journal of Molecular Biology</i> , 2011, 411, 143-157.	4.2	37
27	Identification and analysis of residues contained on $\beta'$ loops of the dual-substrate $(\beta/\beta)_8$ phosphoribosyl isomerase A specific for its phosphoribosyl anthranilate isomerase activity. <i>Protein Science</i> , 2010, 19, 535-543.	7.6	9
28	Protein Design through Systematic Catalytic Loop Exchange in the $(\beta/\beta)_8$ Fold. <i>Journal of Molecular Biology</i> , 2009, 387, 949-964.	4.2	28
29	Enhancement of the Alcoholic Activity of $\beta$ -Amylase AmyA from <i>Thermotoga maritima</i> MSB8 (DSM 3109) by Site-Directed Mutagenesis. <i>Applied and Environmental Microbiology</i> , 2008, 74, 5168-5177.	3.1	15
30	The effect of amino acid deletions and substitutions in the longest loop of GFP. <i>BMC Chemical Biology</i> , 2007, 7, 1.	1.6	15
31	Improvement of an Unusual Twin-Arginine Transporter Leader Peptide by a Codon-Based Randomization Approach. <i>Applied and Environmental Microbiology</i> , 2006, 72, 3797-3801.	3.1	4
32	Generation of variability by in vivo recombination of halves of a $(\beta/\beta)_8$ barrel protein. <i>New Biotechnology</i> , 2005, 22, 113-120.	2.7	1
33	Protein evolution by codon-based random deletions. <i>Nucleic Acids Research</i> , 2004, 32, e136-e136.	14.5	20
34	Combinatorial codon-based amino acid substitutions. <i>Nucleic Acids Research</i> , 2004, 32, e158-e158.	14.5	28
35	Production of a fully functional, permuted single-chain penicillin G acylase. <i>Protein Science</i> , 2004, 13, 1677-1683.	7.6	17
36	A more Efficient Starch Degradation by the Combination of Hydrolase and Transferase Activities of $\beta$ -Amylase and Cyclomaltodextrin Glucanotransferase. <i>Starch/Staerke</i> , 2004, 56, 63-68.	2.1	6

#	ARTICLE	IF	CITATIONS
37	In vivo fragment complementation of a ( $\hat{I}^2/\hat{I}^{\pm}$ )8barrel protein: generation of variability by recombination. <i>FEBS Letters</i> , 2004, 560, 167-172.	2.8	18
38	$\hat{A}$ -Amylase from <i>Bacillus licheniformis</i> mutants near to the catalytic site: effects on hydrolytic and transglycosylation activity. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 505-514.	2.1	40
39	Improving a circularly permuted TEM-1 $\hat{I}^2$ -lactamase by directed evolution. <i>Protein Engineering, Design and Selection</i> , 2002, 15, 463-470.	2.1	30
40	Novel ceftazidime-resistance beta-lactamases generated by a codon-based mutagenesis method and selection. <i>Nucleic Acids Research</i> , 2002, 30, 84e-84.	14.5	12
41	In vivo studies on the positive control function of NifA: a conserved hydrophobic amino acid patch at the central domain involved in transcriptional activation. <i>Molecular Microbiology</i> , 2002, 28, 55-67.	2.5	40
42	Different strategies to recover the activity of monomeric triosephosphate isomerase by directed evolution. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 149-155.	2.1	30
43	Enzymes directly evolving toward commercial applications. <i>Nature Biotechnology</i> , 1999, 17, 539-540.	17.5	1
44	Introducing transglycosylation activity in a liquefying $\hat{I}^{\pm}$ -amylase. <i>FEBS Letters</i> , 1999, 453, 100-106.	2.8	25
45	Microbial sensor for new-generation cephalosporins based in a protein-engineered $\hat{I}^2$ -lactamase. <i>Applied Biochemistry and Biotechnology</i> , 1998, 73, 243-256.	2.9	9
46	Combination of DMT-mononucleotide and Fmoc-trinucleotide phosphoramidites in oligonucleotide synthesis affords an automatable codon-level mutagenesis method. <i>Chemistry and Biology</i> , 1998, 5, 519-527.	6.0	24
47	Temperature-sensitive mutants of the EcoRI endonuclease. <i>Journal of Molecular Biology</i> , 1997, 274, 722-737.	4.2	16
48	Did cyclodextrin glycosyltransferases evolve from $\hat{I}^{\pm}$ -amylases?. <i>FEBS Letters</i> , 1997, 416, 221-224.	2.8	25
49	A proposed architecture for the central domain of the bacterial enhancer-binding proteins based on secondary structure prediction and fold recognition. <i>Protein Science</i> , 1997, 6, 543-555.	7.6	60
50	An Engineered Penicillin Acylase with Altered Surface Charge Is More Stable in Alkaline pH. <i>Annals of the New York Academy of Sciences</i> , 1996, 799, 61-64.	3.8	2
51	Mutant <i>Escherichia coli</i> penicillin acylase with enhanced stability at alkaline pH. <i>Biotechnology and Bioengineering</i> , 1995, 48, 141-148.	3.3	13
52	A New TEM $\hat{I}^2$ -Lactamase Double Mutant with Broadened Specificity Reveals Substrate-dependent Functional Interactions. <i>Journal of Biological Chemistry</i> , 1995, 270, 781-787.	3.4	28
53	Substitution of Asp for Asn at Position 132 in the Active Site of TEM $\hat{I}^2$ -Lactamase. <i>Journal of Biological Chemistry</i> , 1995, 270, 775-780.	3.4	29
54	Saturation mutagenesis of His114 of EcoRI reveals relaxed-specificity mutants. <i>Gene</i> , 1995, 157, 295-301.	2.2	29

#	ARTICLE	IF	CITATIONS
55	Microbial Systems and Directed Evolution of Protein Activities. <i>Critical Reviews in Microbiology</i> , 1994, 20, 107-116.	6.1	9
56	Combinatorial mutagenesis of three major groove-contacting residues of EcoRI: single and double amino acid replacements retaining methyltransferase-sensitive activities. <i>Gene</i> , 1991, 106, 7-12.	2.2	26
57	The Plasmid, pBR322. , 1988, 10, 5-41.		21
58	Plasmid vector pBR322 and its special-purpose derivatives a review. <i>Gene</i> , 1986, 50, 3-40.	2.2	321
59	Construction and characterization of new cloning vehicles V. Mobilization and coding properties of pBR322 and several deletion derivatives including pBR327 and pBR328. <i>Gene</i> , 1981, 13, 25-35.	2.2	163